




Bacterial Whole Genome Sequencing Report

March 29, 2023

Sample ID: SRR17276215

Sequencing Technology

Nextera XT DNA Library Preparation
MiSeq 2 x 250 Read Generation

Sequence Statistics		Quality Scale
		Low  High
Filename	SRR17276215-R1.fastq.gz	SRR17276215-R2.fastq.gz
File size	249.8 MB	335.8 MB
Mean Read Score	34.12	29.64
Q30 Passing	90.2%	64.9%
Sequence Depth	158.2X	Calculated by number of reads x 240/Genome Length
Genome Length	5,000,000bp	Based on MLST identification

Assembly Statistics				Quality Scale		
				Low	<div><div></div></div>	High
Scaffolds	Total length	Longest scaffold	Scaffolds >1K nt	Genome >1K nt	N50	L50
1,811	5,766,508	582,171	56	88.06	224,122	9

De novo assembly performed using SPAdes v3.13.0 .

Multi Locus Sequence Typing (MLST)

Organism ID: **Salmonella enterica** Schema-Sequence type: **senterica_achtman_2-34**

MLST Detail: aroC(10) dnaN(19) hemD(12) hisD(9) purE(5) sucA(9) thrA(2)

Data obtained using 2.23.0. Software website: <https://github.com/tseemann/mlst>

Information on MLST schemes and allelic profiles can be found at pubMLST.org

Serotyping for Salmonella Isolates

Predicted serotype(s) **Typhimurium**
Predicted antigenic profile 4:i:1,2
Predicted subspecies **Salmonella enterica subspecies enterica (subspecies I)**

Note: Detected a deletion in gene oafA that causes O5- variant of Typhimurium.

Data obtained using SeqSero. Software website: <https://github.com/denglab/SeqSero2>

Antimicrobial Resistance Analysis

Results were obtained using [AMRFinder](#). AMRFinder uses BLASTX to search a hierarchy of gene families with predetermined cutoffs.

AMRFinder									
Contig id	Start	Stop	Gene symbol	Sequence name	Scope	% Coverage of reference sequen	% Identity to reference sequen	Class	Subclass
heightNODE_33_length_12022_cov_25.511728	10267	11469	tet(B)	tetracycline efflux MFS transporter Tet(B)	core	100.0	100.0	TETRACYCLINE	TETRACYCLINE
NODE_35_length_9303_cov_541.762533	7419	8060	qnrB19	quinolone resistance pentapeptide repeat protein QnrB19	core	100.0	100.0	QUINOLONE	QUINOLONE
NODE_41_length_4638_cov_109.960763	1990	2802	sul2	sulfonamide-resistant dihydropteroate synthase Sul2	core	100.0	100.0	SULFONAMIDE	SULFONAMIDE
NODE_41_length_4638_cov_109.960763	2842	3666	aph(3'')-Ib	aminoglycoside O-phosphotransferase APH(3'')-Ib	core	100.0	100.0	AMINOGLYCOSIDE	STREPTOMYCIN
NODE_41_length_4638_cov_109.960763	3669	4502	aph(6)-Id	aminoglycoside O-phosphotransferase APH(6)-Id	core	100.0	100.0	AMINOGLYCOSIDE	STREPTOMYCIN
NODE_47_length_2168_cov_46.195982	663	1520	blaTEM-1	broad-spectrum class A beta-lactamase TEM-1	core	100.0	100.0	BETA-LACTAM	BETA-LACTAM

AMRFinder

Revision 3.10.16

<https://github.com/ncbi/amr/wiki>

Definitions were taken from the AMRFinder documentation.

Target Identifier- This is from the FASTA define for the DNA sequence

Contig id- Contig name

Start- 1-based coordinate of first nucleotide coding from protein in DNA sequence on contig

Stop- 1-based coordinate of last nucleotide coding for protein in DNA sequence on contig

Gene symbol- Gene or gene-family symbol for protein hit

Protein name- Full-text name for the protein

Method- Type of hit found by AMRFinder one of five options

ALLELE- 100% sequence match over 100% of length to a protein named at the allele level in the AMRFinder database

EXACT- 100% sequence match over 100% of length to a protein in the database that is not a named allele

BLAST- BLAST alignment is >90% of length and >90% identity to a protein in a the AMRFinder database

PARTIAL- BLAST alignment is >50% of length, but <90% of length and >90% identity

HMM- HMM was hit above the cutoff, but there was not a BLAST hit that met standards for BLAST or PARTIAL

Target length- The length of the query protein. The length of the BLAST hit for translated-DNA searches

Reference protein length- The length of the AMR Protein in the database (NA if HMM-only hit)

% Coverage of reference protein- % covered by blast hit (NA if HMM-only hit)

% Identity to reference protein- % amino-acid identity to reference protein (NA if HMM-only hit)

Alignment length- Length of BLAST alignment in amino acids (NA if HMM-only hit)

Accession of closest protein- RefSeq accession for protein hit by BLAST (NA if HMM-only hit)

Name of closest protein- Full name assigned to the AMRFinder database protein (NA if HMM-only hit)

HMM id- Accession for the HMM

HMM description- The family name associated with the HMM